

EXHIBIT 2

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## Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

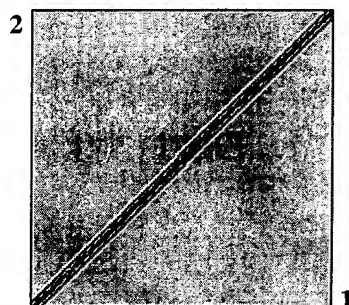
Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.15 [Oct-15-2006]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**  
x\_dropoff: **50** expect: **10.0000** wordsize: **3** Filter ☐ View option **Standard**  
Masking character option **X for protein, n for nucleotide** Masking color option **Black**  
☐ Show CDS translation **Align**

**Sequence 1:** gi|1469860|dbj|BAA09787.1|leptin [Homo sapiens] >gi|4557715|ref|NP\_000221.1| leptin precursor [Homo sapiens] >gi|730218|sp|P41159|LEP\_HUMAN Leptin precursor (Obesity factor) (Obese protein)  
>gi|623332|gb|AAA60470.1| ob >gi|1226244|gb|AAC50400.1| obese protein >gi|1407583|dbj|BAA09839.1| ob protein  
[Homo sapiens] >gi|38174530|gb|AAH60830.1| Leptin (obesity homolog, mouse) [Homo sapiens]  
>gi|46854318|gb|AAH69527.1| Leptin (obesity homolog, mouse) [Homo sapiens] >gi|46854679|gb|AAH69452.1| Leptin  
(obesity homolog, mouse) [Homo sapiens]...  
Length = 167 (1 .. 167)

**Sequence 2:** gi|87196505|ref|NP\_776353.2|leptin [Bos taurus] >gi|59857615|gb|AAX08642.1| leptin precursor [Bos taurus]  
Length = 167 (1 .. 167)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 274 bits (701), Expect = 1e-72  
Identities = 141/167 (84%), Positives = 151/167 (90%), Gaps = 0/167 (0%)

Query	1	MHWGTLCGFLWLWPYLFYVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVVTGL	60
		M G L FLWLWPYL YV+AVPI KVQDDTKTLIKTIVTRINDISHTQSVSSKQ+VTGL	
Sbjct	1	MRCGPLYRFLWLWPYLSYVEAVPICKVQDDTKTLIKTIVTRINDISHTQSVSSKQQRVTGL	60
Query	61	DFIPGLHPILTL SKMDQTLAVYQQILTSMP SRNVIQISNDLENLRDLLHVLAFSKSCHLP	120
		DFIPGLHP+L+LSKMDQTLA+YQQILTS+PSRNV+QISNDLENLRDLLH+LA SKSC LP	
Sbjct	61	DFIPGLHPLL SL SKMDQTLAIYQQILTS LPSRNVVQISNDLENLRDLLHLLAASKSCPLP	120
Query	121	WASGLETLDL SGGVLEASGYSTEVVALSRLQGS LQDMLQDL DSPGC	167
		LE+L+SLG VLEAS YSTEVVALSRLQGS LQDML QDL DSPGC	
Sbjct	121	QVRALESLES LGVVLEASLYSTEVVALSRLQGS LQDMLQDL DSPGC	167

CPU time: 0.02 user secs. 0.01 sys. secs 0.03 total secs.

Lambda	K	H
0.321	0.135	0.415

## Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 279

Number of extensions: 96

Number of successful extensions: 1

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 167

Length of database: 1,565,033,500

Length adjustment: 124

Effective length of query: 43

Effective length of database: 1,565,033,376

Effective search space: 67296435168

Effective search space used: 67296435168

Neighboring words threshold: 9

X1: 16 ( 7.4 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.9 bits)

S2: 73 (32.7 bits)